

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/573,999
Source: 1FWP
Date Processed by STIC: 4/13/06

ENTERED



IFWP

RAW SEQUENCE LISTING

DATE: 04/13/2006

PATENT APPLICATION: US/10/573,999

TIME: 10:01:02

Input Set : A:\BCS 03-5005_PCT-SEQUENZPROTOKOLL.ST25.txt

Output Set: N:\CRF4\04132006\J573999.raw

3 <110> APPLICANT: Bayer CropScience GmbH
 5 <120> TITLE OF INVENTION: Plants with increased activity of a Class 3 branching enzyme
 7 <130> FILE REFERENCE: BCS 03-5005-PCT
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/573,999
 C--> 9 <141> CURRENT FILING DATE: 2006-03-30
 9 <150> PRIOR APPLICATION NUMBER: EP 03090324.9
 10 <151> PRIOR FILING DATE: 2003-09-30
 12 <160> NUMBER OF SEQ ID NOS: 6
 14 <170> SOFTWARE: PatentIn version 3.1
 16 <210> SEQ ID NO: 1
 17 <211> LENGTH: 1004
 18 <212> TYPE: DNA
 19 <213> ORGANISM: Solanum tuberosum
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 42 ttgcttggaa gtgcctctgc caagtagaag tgctcaggtc tacaagttga cccgaattct 660
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 67 cggggtcga gtttcgaggt gtagatgctc agcaacggag caaccgccac cgcaacgacg 180
 69 gaagcaacga cgggagaagt acaaacagtc ggaggaaggg aaaggaatcg atcctgttgg 240
 71 atttctcagc aaatacggca ttactcataa agcgtttgct caatttcttc gtgaaagata 300
 73 taaatcattg aaggacttga aggatgaaat attgactcgt catttcagtc tcaaggagat 360
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83 caattatgcg gaggactatg gtaaagggtga cacgggtatt accgtcgagg aaatctttaa 660
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89 actagaagca atgcctgatg cagctacacg atacaaaact tggaaagagc aacaaaaaga 840
91 ggatccggca agcaatttgc catcgatga tgtggtagat agtggaaaag aatatgatat 900
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141 <222> LOCATION: (99)..(2804)
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149 Met Leu Ser Leu Ser Asp
150 1 5
152 tca att cga att tct tca cca ttg agc gat tct cgt ctt agt ttt cta 164
153 Ser Ile Arg Ile Ser Ser Pro Leu Ser Asp Ser Arg Leu Ser Phe Leu
154 10 15 20
156 tct caa acc gga agc aga acc agt cgc cag ctt aaa ttt gtt cgc agc 212
157 Ser Gln Thr Gly Ser Arg Thr Ser Arg Gln Leu Lys Phe Val Arg Ser
158 25 30 35
160 cgc cgg gct cga gtt tcg agg tgt aga tgc tca gca acg gag caa ccg 260
161 Arg Arg Ala Arg Val Ser Arg Cys Arg Cys Ser Ala Thr Glu Gln Pro
162 40 45 50

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166	55				60					65						70	
168	gaa	gag	aaa	gga	atc	gat	cct	gtt	gga	ttt	ctc	agc	aaa	tac	ggc	att	356
169	Glu	Glu	Lys	Gly	Ile	Asp	Pro	Val	Gly	Phe	Leu	Ser	Lys	Tyr	Gly	Ile	
170					75					80						85	
172	act	cat	aaa	gcg	ttt	gct	caa	ttt	ctt	cgt	gaa	aga	tat	aaa	tca	ttg	404
173	Thr	His	Lys	Ala	Phe	Ala	Gln	Phe	Leu	Arg	Glu	Arg	Tyr	Lys	Ser	Leu	
174				90						95						100	
176	aag	gac	ttg	aag	gat	gaa	ata	ttg	act	cgt	cat	ttc	agt	ctc	aag	gag	452
177	Lys	Asp	Leu	Lys	Asp	Glu	Ile	Leu	Thr	Arg	His	Phe	Ser	Leu	Lys	Glu	
178			105							110						115	
180	atg	tct	act	ggg	tat	gaa	tta	atg	ggt	atg	cat	cgc	aac	ata	caa	cat	500
181	Met	Ser	Thr	Gly	Tyr	Glu	Leu	Met	Gly	Met	His	Arg	Asn	Ile	Gln	His	
182			120							125						130	
184	cga	gtg	gat	ttc	ttg	gaa	tgg	gct	cca	ggt	gct	cgc	tac	tgt	gct	ctg	548
185	Arg	Val	Asp	Phe	Leu	Glu	Trp	Ala	Pro	Gly	Ala	Arg	Tyr	Cys	Ala	Leu	
186	135					140						145				150	
188	att	ggt	gac	ttc	aat	ggg	tgg	tca	aca	act	ggt	aac	tgt	gcc	aga	gag	596
189	Ile	Gly	Asp	Phe	Asn	Gly	Trp	Ser	Thr	Thr	Gly	Asn	Cys	Ala	Arg	Glu	
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192	ggt	cat	ttt	ggt	cat	gac	gat	tat	ggg	tat	tgg	ttt	att	att	ctt	gaa	644
193	Gly	His	Phe	Gly	His	Asp	Asp	Tyr	Gly	Tyr	Trp	Phe	Ile	Ile	Leu	Glu	
194				170						175						180	
196	gat	aaa	tta	cgt	gaa	gga	gaa	gaa	cct	gat	aaa	ttg	tat	ttt	caa	cag	692
197	Asp	Lys	Leu	Arg	Glu	Gly	Glu	Glu	Pro	Asp	Lys	Leu	Tyr	Phe	Gln	Gln	
198			185							190						195	
200	tac	aat	tat	gcg	gag	gac	tat	gat	aaa	ggt	gac	acg	ggt	att	acc	gtc	740
201	Tyr	Asn	Tyr	Ala	Glu	Asp	Tyr	Asp	Lys	Gly	Asp	Thr	Gly	Ile	Thr	Val	
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204	gag	gaa	atc	ttt	aaa	aaa	gca	aat	gat	gag	tat	tgg	gaa	cct	gga	gaa	788
205	Glu	Glu	Ile	Phe	Lys	Lys	Ala	Asn	Asp	Glu	Tyr	Trp	Glu	Pro	Gly	Glu	
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208	gat	cgc	ttc	att	aaa	tca	cgt	tat	gag	gtg	gca	gca	aag	tta	tat	gag	836
209	Asp	Arg	Phe	Ile	Lys	Ser	Arg	Tyr	Glu	Val	Ala	Ala	Lys	Leu	Tyr	Glu	
210					235					240						245	
212	gaa	atg	ttc	gga	cca	aat	gga	cct	caa	aca	gaa	gag	gaa	cta	gaa	gca	884
213	Glu	Met	Phe	Gly	Pro	Asn	Gly	Pro	Gln	Thr	Glu	Glu	Glu	Leu	Glu	Ala	
214				250						255						260	
216	atg	cct	gat	gca	gct	aca	cga	tac	aaa	act	tgg	aaa	gag	caa	caa	aaa	932
217	Met	Pro	Asp	Ala	Ala	Thr	Arg	Tyr	Lys	Thr	Trp	Lys	Glu	Gln	Gln	Lys	
218				265						270						275	
220	aag	gat	ccg	gca	agc	aat	ttg	cca	tcg	tat	gat	gtg	gta	gat	agt	gga	980
221	Lys	Asp	Pro	Ala	Ser	Asn	Leu	Pro	Ser	Tyr	Asp	Val	Val	Asp	Ser	Gly	
222			280									290					
224	aaa	gaa	tat	gat	att	tac	aat	att	ata	ggt	gat	cct	gaa	tcg	ttt	aag	1028
225	Lys	Glu	Tyr	Asp	Ile	Tyr	Asn	Ile	Ile	Gly	Asp	Pro	Glu	Ser	Phe	Lys	
226	295					300					305					310	
228	aaa	ttt	cgt	atg	aaa	cag	cct	cct	att	gct	tac	tgg	tta	gaa	act	aaa	1076

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236 gga agc aaa cac agg gtg tat ttt aac aca cca aat ggg cct ctt gaa      1172
237 Gly Ser Lys His Arg Val Tyr Phe Asn Thr Pro Asn Gly Pro Leu Glu
238          345          350          355
240 cga gtt cct gcg tgg gcc aat ttt gtc att cca gat gca gac ggg atg      1220
241 Arg Val Pro Ala Trp Ala Asn Phe Val Ile Pro Asp Ala Asp Gly Met
242          360          365          370
244 gca tta gca gtc cat tgg gaa cca cct cct gaa tat gct tat aaa tgg      1268
245 Ala Leu Ala Val His Trp Glu Pro Pro Pro Glu Tyr Ala Tyr Lys Trp
246 375          380          385          390
248 aaa cac aag cta cca gtc aag cct aag tcc ttg cgc ata tat gaa tgt      1316
249 Lys His Lys Leu Pro Val Lys Pro Lys Ser Leu Arg Ile Tyr Glu Cys
250          395          400          405
252 cat gtt ggc atc tct ggc cag gaa cca aaa gtt tca tct ttc aat gat      1364
253 His Val Gly Ile Ser Gly Gln Glu Pro Lys Val Ser Ser Phe Asn Asp
254          410          415          420
256 ttt att agc aag gtc ctt ccg cat gta aaa gaa gct gga tac aat gca      1412
257 Phe Ile Ser Lys Val Leu Pro His Val Lys Glu Ala Gly Tyr Asn Ala
258          425          430          435
260 acg caa att att gga gtt gtt gag cac aag gat tat ttc act gtt gga      1460
261 Thr Gln Ile Ile Gly Val Val Glu His Lys Asp Tyr Phe Thr Val Gly
262          440          445          450
264 tat aga gtg acc aat ttt tat gct gtt agt agc cgt tat ggc aca ccg      1508
265 Tyr Arg Val Thr Asn Phe Tyr Ala Val Ser Ser Arg Tyr Gly Thr Pro
266 455          460          465          470
268 gat gac ttc aag cgc ttg gtt gat gaa gca cat ggg ctt gga ctg ctt      1556
269 Asp Asp Phe Lys Arg Leu Val Asp Glu Ala His Gly Leu Gly Leu Leu
270          475          480          485
272 gtc ttt ttg gag att gtg cac tcc tat gca gca gca gat gaa atg gtt      1604
273 Val Phe Leu Glu Ile Val His Ser Tyr Ala Ala Ala Asp Glu Met Val
274          490          495          500
276 ggg tta tct ctt ttt gat gga gca aat gat tgc tat ttc cac act ggt      1652
277 Gly Leu Ser Leu Phe Asp Gly Ala Asn Asp Cys Tyr Phe His Thr Gly
278          505          510          515
280 aaa cgt gga cac cac aaa ttc tgg ggc aca cgg atg ttc aaa tat gga      1700
281 Lys Arg Gly His His Lys Phe Trp Gly Thr Arg Met Phe Lys Tyr Gly
282          520          525          530
284 gat cct gat gtt ctg cac ttt ctt ctt tca aat ctg aac tgg tgg gtg      1748
285 Asp Pro Asp Val Leu His Phe Leu Leu Ser Asn Leu Asn Trp Trp Val
286 535          540          545          550
288 gag gag tat cat gtc gat ggc ttc cat ttt cat tcg ctc tcg tcc atg      1796
289 Glu Glu Tyr His Val Asp Gly Phe His Phe His Ser Leu Ser Ser Met
290          555          560          565
292 ttg tat acg cat aat gga ttt gct tca ttt act ggt gac atg gat gaa      1844
293 Leu Tyr Thr His Asn Gly Phe Ala Ser Phe Thr Gly Asp Met Asp Glu

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298	585	590	595	
300 gca aat gaa gta tta cat gct ctt cat cct aat gtg atc acg att gct	1940			
301 Ala Asn Glu Val Leu His Ala Leu His Pro Asn Val Ile Thr Ile Ala				
302	600	605	610	
304 gtg gat gca act ctg tat cct gga ctc tgc gat cca aca tct caa ggt	1988			
305 Val Asp Ala Thr Leu Tyr Pro Gly Leu Cys Asp Pro Thr Ser Gln Gly				
306 615	620	625	630	
308 gga ctg ggc ttt gat tat ttt gcc aat ctt tct gcc tca gag atg tgg	2036			
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310	635	640	645	
312 ctt gca tta ctt gaa aat act cct gat cat gaa tgg tgc atg agt aag	2084			
313 Leu Ala Leu Leu Glu Asn Thr Pro Asp His Glu Trp Cys Met Ser Lys				
314	650	655	660	
316 att gtt agc aca tta gtg ggc gat aga caa aat act gat aaa atg ctt	2132			
317 Ile Val Ser Thr Leu Val Gly Asp Arg Gln Asn Thr Asp Lys Met Leu				
318	665	670	675	
320 ttg tat gca gaa aat cac aac cag tcc att tct gga ggt cgt tcc ttc	2180			
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322	680	685	690	
324 gca gaa ata ctg att ggt aac tcc ttg ggg aaa tct tcc ata tca caa	2228			
325 Ala Glu Ile Leu Ile Gly Asn Ser Leu Gly Lys Ser Ser Ile Ser Gln				
326 695	700	705	710	
328 gag tca tta ctt aga ggc tgc tcg tta cac aag atg atc aga tta att	2276			
329 Glu Ser Leu Leu Arg Gly Cys Ser Leu His Lys Met Ile Arg Leu Ile				
330	715	720	725	
332 aca tct aca att ggt ggt cat gca tac ctc aac ttc atg ggc aat gaa	2324			
333 Thr Ser Thr Ile Gly Gly His Ala Tyr Leu Asn Phe Met Gly Asn Glu				
334	730	735	740	
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338	745	750	755	
340 tcc ttt tca ctg gct aac cgt cgc tgg gat cta ttg gaa gat gtt gta	2420			
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354	810	815	820	
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VERIFICATION SUMMARY

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L:9 M:270 C: Current Application Number differs, Replaced Current Application No

L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date